# Molecular characterization of *Euphorbia caput-medusae stunt virus*: evidence for the existence of a new genus within the family *Geminiviridae*

Bernardo P.[1], Fernandez E.[1], Granier M.[1], Golden M.[2], Rebelo T.[3], Peterschmitt M.[1], Martin DP. [2], Roumagnac P. [1]

[1] CIRAD-INRA-SupAgro. UMR BGPI, TA A-54/K, Campus International de Baillarguet, F-34398 Montpellier Cedex 5. Email: pauline.bernardo@supagro.inra.fr
[2] Werner Beit South Building; S3.26. Institute of Infectious Disease and Molecular Medicine. UCT Faculty Of Health Sciences. Observatory 7925. South Africa
[3] South African National Biodiversity Institute, Kirstenbosch, Private Bag X7, Claremont 7735, Cape Town, South Africa

pauline.bernardo@supagro.inra.fr

Studies focusing on phytoviruses isolated from the wild are rare. Nevertheless, even if those studies remain scarce, it is increasingly accepted that viruses coming from wild plants might play a role on disease emergence and in the functioning of ecosystems. Geminivirus are a major cause of disease on plants of agronomic interest. We hypothesize that strengthening our knowledge of the geminivirus diversity coming from the wild could help reconstructing the evolutionary history of the *Geminiviridae* family but also could help us understanding and predicting future epidemics.

Over the past two decades, rolling circle amplification (RCA) has been more and more employed for the detection of small circular single-stranded DNA viruses, including geminivirus coming from the wild [1]. We have used this method for detecting the presence of ssDNA from 236 plants collected in the South African fynbos. We have obtained amplified DNAs from 36% of the plants (85 out of 236 plants). Using classical cloning and sequencing methods, we have obtained ten sequences of which one was identified as a plant virus. This viral sequence corresponds to a new geminivirus, which infects a wild spurge (*Euphorbia caput-medusae*). This geminivirus is highly divergent from the current known members of the family *Geminiviridae* and is likely to represent a new previously unknown genus of this agriculturally highly relevant family of viruses. The virus, which we have named *Euphorbia caput-medusae stunt virus* (EcmSV) is not obviously a recombinant of viruses in the known geminivirus genera, has features most similar to viruses in the genus *Mastrevirus* (the presence of a *repA* gene and the production transcripts that are almost certainly spliced), but it also has unique features among geminiviruses (potential product of spliced V2-V3 ORFs). Besides EcmSV providing new information on the evolutionary history of geminiviruses, its discovery stresses the need to better assess viral diversity at the interface between wild and cultivated areas (by *in situ* sampling) and to study viruses isolated from wild hosts for their potential to infect crop species and *vice-versa* (by *in vitro* experimentation).

1. Varsani,A. *et al.* A highly divergent South African geminivirus species illuminates the ancient evolutionary history of this family. *Virol. J* **6**, 36 (2009).